

GenCore version 5.1.3  
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## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 14, 2003, 02:07:45 ; Search time 92.2921 Seconds  
(without alignments)  
1579.326 Million cell updates/sec

Title: US-09-698-781-17  
Perfect score: 44  
Sequence: 1 TLFPPVLLFL 9

Scoring table: BL2USUM62  
Xgapext 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Command line parameters:

```
-MODEL=frame+_p2n.model -DEV=x1h
-O=cgn2_1/uspro_spool/usr/06988781/runat_07032003_083459_5329/app_query.fasta_1.654
-DB=EST -OFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=bl2usum62 -TRANS=human40_cdi -LIST=45
-DODCALIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=15 -MODE=LOCAL
-OUTPMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09698781@CCN_1_2465_@runat_07032003_083459_5329 -NCPU=6 -TIPU=3
-NO_XLPPY -NO_NMAP -LARGSEQURY -NEG SCORES=0 -WAIT -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

## Database :

EST : \*

```
1: em_lestba:*
2: em_lethum:*
3: em_lestin:*
4: em_lestmu:*
5: em_lestov:*
6: em_lestpl:*
7: em_lestro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pch:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rnd:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	10.0	547	9 AL703262	AL703262 DKFPZp686K
2	42	95.5	353	14 BQ966605	BQ966605 QHB2Pf16.
3	41	93.2	308	14 BM832007	BM832007 K-EST0106
4	41	93.2	407	14 BM822727	BM822727 K-EST0092
5	41	93.2	447	10 AW009767	AW009767 ws87099.x
6	41	93.2	461	10 BB839116	BB839116 BB839116
7	41	93.2	538	14 BN751298	BN751298 K-EST0027
8	41	93.2	575	10 MO20302 M	BE016163 AZ10844 RPCI-23-4
9	41	93.2	619	17 AZ108486	AU138699 AU138699
10	41	93.2	693	9 AU138699	AU138699 AU138699
11	41	93.2	722	12 BG772279	BG772279 602656263
12	41	93.2	724	10 BE545083	BE545083 601077815
13	41	93.2	767	13 BN013479	BN013479 603638933
14	41	93.2	785	14 BM715733	BM715733 E-E-EJ0
15	41	93.2	813	12 BG574770	BG574770 602556822
16	41	93.2	861	14 BQ441085	BQ441085 AGENCOURT
17	41	93.2	869	17 A2539955	A2539955 ENTES337TF
18	41	93.2	898	17 A2669486	A2669486 ENTAN76T
19	41	93.2	921	17 BR132102	BR132102 ENTPB47-TF
20	41	93.2	972	14 BQ071051	BQ071051 AGENCOURT
21	41	93.2	1018	14 BQ052048	BQ052048 AGENCOURT
22	41	93.2	1072	14 BQ052048	BQ052048 AGENCOURT
23	41	93.2	1075	14 BQ06922	BQ06922 AGENCOURT
24	41	93.2	1094	12 BG18306	BG18306 602350108
25	41	93.2	1117	10 BB372269	BB372269 601223588
26	41	93.2	1187	17 A2686289	A2686289 ENTKUT4TF
27	40	90.9	349	13 BI178406	BI178406 EST519351
28	40	90.9	421	10 BE17732	BE17732 RCI-RT059
29	40	90.9	469	17 AQ203941	AQ203941 HS-3340_A
30	40	90.9	578	17 A2849527	A2849527 2M015JC06
31	40	90.9	643	14 BQ120863	BQ120863 EST60439
32	40	90.9	656	14 BQ509628	BQ509628 EST617043
33	40	90.9	659	10 BB344289	BB344289 BB344289
34	40	90.9	955	17 CNS7017	CNS7017 end of
35	39	88.6	103	9 A1956273	A1956273 uJ73b11.Y
36	39	88.6	105	17 A2828001	A2828001 2M0104F13
37	39	88.6	186	9 A157293	A157293 le39d11.x
38	39	88.6	192	12 BB819364	BB819364 IL0-RY001
39	39	88.6	270	17 TA383801Q	TA383801Q AL49765_T_brucei
40	39	88.6	297	17 BB82165	BB82165 PCP11_26D7
41	39	88.6	309	12 BF331555	BF331555 RC0-BP056
42	39	88.6	318	12 BF879720	BF879720 RC2-EY018
43	39	88.6	334	9 AB883350	AB883350 d445C10.S
44	39	88.6	340	9 AA007134	AA007134 3JcDNA3
45	39	88.6	342	10 BB870337	BB870337 BB870337

## ALIGNMENTS

RESULT 1  
AL703262 LOCUS AL703262 mRNA linear EST 22-MAR-2002  
DEFINITION DKFPZp686K1819\_r1\_686 (synonym: hlc3c3) Homo sapiens cDNA clone  
ACCESSION AL703262  
VERSION AL703262.1 GI:19486617  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE (bases 1 to 547)  
1 Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.).  
AUTHORS EST (Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann  
TITLE

JOURNAL	,S.) Unpublished (1999)	tel: 1-(530)-742-1742 Fax: 1-(530)-752-9659 Email: akozik@agc.org [michelmore@gmail.ucdavis.edu] singleton; http://cgpdbs.ucdavis.edu/ for details.
COMMENT	Contact: Poustka A.J. Department Lehrsch Max-Planck Institute for Molecular Genetics Innestrasse 73, 14195 Berlin, Germany Tel: +49-30-84131623 Fax: +49-30-84131128	Plate: QHB27 row: F column: 16. Location/Qualifiers
FEATURES	source	1..353 /organism="Helianthus annuus" /cultivar="RHA801" /db_xref="taxon:9606" /clone="QHB27F16" /clone_id="OH_ABCDI sunflower RHA801" /lab_host="E.coli" /note="Vector: PRCDNNSF1AB: The library was constructed from 11 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdbs.ucdavis.edu/ TAG_LIN=OH ABCDI sunflower RHA801
FEATURES	source	1..547 /organism="Homo sapiens" /note="vector: pTREipleX2; site_1: SfI1A; site_2: SfI1B; cdna-collection" BASE COUNT
ORIGIN	170 a 120 c 120 g 137 t	/note="vector: pTREipleX2; site_1: SfI1A; site_2: SfI1B; cdna-collection" Alignment Scores: Pred. No.: 373 Length: 547 Score: 44.00 Matches: 9 Percent Similarity: 100.00% Conservative: 1 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 9 Indels: 0 DB: Gaps: 0
US-09-698-781-17 (1-9) x AL703262 (1-547)		
QY	1 ThrieupPhrovalleleuPhreleu 9	
DB	46 ACATTTATCCCGAGCTGTTCTG 72	
RESULT 2		
BQ966605/c	BQ966605 353 bp mRNA linear EST 21-AUG-2002	
LOCUS	QHB27F16.yg abl OH_ABCDI sunflower RHA801 Helianthus annuus cDNA	
DEFINITION	clone QHB27F16, mRNA sequence.	
ACCESSION	BQ966605	
VERSION	1 GI:22383710	
KEYWORDS	EST.	
SOURCE	common sunflower.	
ORGANISM	Helianthus annuus	
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae; Heliantheae; Helianthus.	
REFERENCE	1 (bases 1 to 353)	
TITLE	Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Riesenberg, L., Lin, H., van Damme, J., Lavelle, D., Chevalier, P., Ziedie, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Tai, Z., Church, S., Jackson, L. and Bradford, K.	
TITLE	Lettuce and Sunflower ESTs from the Compositae Genome Project	
http://compgenomics.ucdavis.edu/		
COMMENT	Unpublished (2002) Contact: Alexander Kozik [R.W.Michelmore] Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Asmundson Hall, UCD, Davis, CA 95616, USA	
JOURNAL		
COMMENT		
FEATURES	source	High quality sequence stop: 08 Location/Qualifiers 1..308 /organism="Homo sapiens" /db_xref="taxon:9606"

/clone="S20t665307-32-C08"

/clone\_1.lib="S20t665307"

/sex="M"

/lab\_host="Top10F"

/note="Organ: Stomach; Vector: pcNS; Site\_1: EcoRI;

Site\_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped

with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR

I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by

priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was

circularized with E. coli DNA ligase after digestion of

EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The

obtained cDNA vectors were used for transformation of

competent cells E. coli Top10F' by electroporation method.

The cDNA libraries constructed by this method are

full-length enriched cDNA library."

BASE COUNT 117 a 54 c 99 g 38 t

ORIGIN

Alignment Scores:

Pred. No.: 629 Length: 308

Score: 41.00 Matches: 8

Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 88.89% Mismatches: 0

Query Match: 93.18% Indels: 0

DB: 14 Gaps: 0

US-09-698-781-17 (1-9) x BM832007 (1-308)

QY 1 ThrLeuPheProValLeuLeuPheLeu 9

Db 133 ACTCTCTTCCTCTCTTTCTT 107

RESULT 4 BM822727/c

LOCUS K-BEST092951 S20t665307 Homo sapiens mRNA clone S20t665307-17-H07

DEFINITION 5', mRNA sequence.

ACCESSION BM822727

VERSION 1.1 G1:19179140

KEYWORDS EST.

SOURCE human.

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 407)

AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,

Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and

Kim,Y.S.

TITLE CIC Frontier Korean EST Project 2001

JOURNAL Unpublished

COMMENT Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Baeun-dong Yusung-gu, Daejon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 17 Row: H Column: 07

High quality sequence stop: 407.

FEATURES source

1. .407

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:2504921"

/clone\_1.lib="NCL\_CGAP\_CO3"

/sex="pooled"

/tissue\_type="colon"

/lab\_host="DH10B"

/note="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA

was prepared from 12 pooled bulk tumor samples and primed

with a Not I - oligo(dT) primer. Double-stranded cDNA was

Site\_2: NotI: The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped

intact mRNA was ligated with DNA-RNA linker including EcoR

I site by treatment of T4 RNA ligase and the first strand

cDNA was synthesized from oligo dT-selected mRNA by

priming with dT-tailed vector. The dT-tailed vector was

adjusted to have about 60nt. The cDNA vector was

circularized with E. coli DNA ligase after digestion of

EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The

obtained cDNA vectors were used for transformation of

competent cells E. coli Top10F' by electroporation method.

The cDNA libraries constructed by this method are

full-length enriched cDNA library."

BASE COUNT 132 a 85 c 129 g 61 t

ORIGIN

Alignment Scores:

Pred. No.: 889 Length: 407

Score: 41.00 Matches: 8

Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 88.89% Mismatches: 0

Query Match: 93.18% Indels: 0

DB: 14 Gaps: 0

US-09-698-781-17 (1-9) x BM822727 (1-407)

QY 1 ThrLeuPheProValLeuLeuPheLeu 9

Db 71 ACTCTCTTCCCTCTCTTCTT 45

RESULT 5 AW009767/c

LOCUS AW009767 ws81b09.x1 NCL\_CGAP\_CO3 Homo sapiens mRNA clone IMAGE:2504921 3'

DEFINITION mRNA sequence.

ACCESSION AW009767

VERSION 1.1 G1:5859545

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 447)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP Title National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL Tumor Gene Index

Unpublished (1997)

COMMENT Upload: Robert Strausberg, Ph.D.

Email: cgaps@mail.nih.gov

Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arraying: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone Distribution: NCI-CGAP clone distribution information can be

found through the I. M. A. G. E. Consortium/LLNL at: www.bio.llnl.gov/bcrp/image/image.html

Seq Primer: -40up from Gibco.

Location/Qualifiers

FEATURES source

1. .447

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:2504921"

/clone\_1.lib="NCL\_CGAP\_CO3"

/sex="M"

/lab\_host="Top10F"

/note="Organ: Stomach; Vector: pcNS; Site\_1: EcoRI;"

BASE COUNT	171 a	67 c	70 g	139 t	FEATURES	e mouse tissues.
ORIGIN					SOURCE	Location/Qualifiers
PRED. NO.:	998	Length:	447			1. . 461
SCORE:	41.00	Matches:	8	/organism="Mus musculus"		
PERCENT SIMILARITY:	100.00%	Conservative:	1	/strain="C57BL/6J"		
BEST LOCAL SIMILARITY:	88.89%	Mismatches:	0	/db_xref="Taxon:10990"		
QUERY MATCH:	93.18%	Indels:	0	/clone="BB60007012"		
DB:	10	Gaps:	0	/clone_id="RIKEN full-length enriched, 8 cells embryo"		
RESULT	6			/cell_type="8 cells"		
LOCUS	BB839116	461 bp	mRNA	/dev_stage="8 cells embryo"		
DEFINITION	BB839116 RIKEN full-length enriched, 8 cells embryo	linear	EST	/note="vector: pSPORT1; Site 1: Sali; Site 2: NotI; This		
CDNA CLONE	E890007012 5'	8 cells	embryo	clone is among a rearranged set of 15,247 clones from 11		
ACCESSION	BB839116	mRNA sequence.		embryo cDNA libraries (including preimplantation stage		
VERSION	BB839116.1	GI:17039847		embryos from unfertilized egg to blastocyst, embryonic		
EST.				part of E7.5 embryos, extraembryonic part of E7.5 embryos		
SOURCE	house mouse.			, and E12.5 female mesonephros/gonad) and one newborn		
ORGANISM	Mus musculus			ovary cDNA library. Average insert size 1.5 kb. All		
EUKARYOTA: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;				source libraries are cloned unidirectionally with Oligo(dT		
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				)-Not Primers. References include: (1) Genome-wide		
REFERENCE	1 (bases 1 to 461)			expression profiling of mid-gestation placenta and embryo		
AUTHORS	Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanashiki,T., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsumaya,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sekai,C., Sekai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tazawa,A., Takahashi,F., Takaku-Akohira,S., Tanaka,T., Tomaru,A., Toya,T., Watanuki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.			using a 15,000 mouse developmental cDNA microarray, 2000,		
TITLE	RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al. 2001)			Large-scale cDNA analysis reveals phased gene expression		
JOURNAL	Unpublished (2001)			patterns during preimplantation mouse development, 2000,		
COMMENT	Contact: Yoshinide Hayashizaki			Development, 127: 1737-1749; (3) Genome-wide mapping of		
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute of Physical and Chemical Research (RIKEN)				unselected transcripts from extraembryonic tissue of		
The Institute of Physical and Chemical Research (RIKEN)				7.5 day mouse embryos reveals enrichment in the t-complex		
1-7-22 Siehoro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan				and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."		
TEL: 81-45-503-9222				Mol Genet 7: 1967-1978."		
FAX: 81-45-503-9215						
Email: genome-res@gsc.riken.go.jp/						
URL: http://genome.gsc.riken.go.jp/						
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.						
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res.: 10 (10), 1617-1630 (2000)						
Wada,K., Fujikawa,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.						
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res.: 10 (11), 1757-1771 (2000)						
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.						
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res.: 11 (2), 281-289 (2001)						
Please visit our web site ( <a href="http://genome.gsc.riken.go.jp">http://genome.gsc.riken.go.jp</a> ) for further details.						

RESULT	7	Alignment Scores:		FEATURES	e mouse tissues.
LOCUS	BM751298	Length:	461	SOURCE	Location/Qualifiers
DEFINITION	K-EST0027348 s9snu01 Homo sapiens	Matches:	8		1. . 461
ACCESSION	BM751298	Conservative:	1	/organism="Mus musculus"	
VERSION	BM751298.1	Mismatches:	0	/strain="C57BL/6J"	
KEYWORDS	EST.	Indels:	0	/db_xref="Taxon:10990"	
SOURCE	human.	Gaps:	0	/clone="BB60007012"	
ORGANISM	Homo sapiens			/clone_id="RIKEN full-length enriched, 8 cells embryo"	
EUKARYOTA: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.				/cell_type="8 cells"	
REFERENCE	1 (bases 1 to 538)			/dev_stage="8 cells embryo"	
AUTHORS	Kim,N.S., Hahn,K.Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.			/note="vector: pSPORT1; Site 1: Sali; Site 2: NotI; This	
TITLE	21C Frontier Korean EST Project 2001			clone is among a rearranged set of 15,247 clones from 11	
JOURNAL	Unpublished (2002)			embryo cDNA libraries (including preimplantation stage	
COMMENT	Contact: Kim YS			embryos from unfertilized egg to blastocyst, embryonic	
Korea Research Institute of Bioscience & Biotechnology				part of E7.5 embryos, extraembryonic part of E7.5 embryos	
52 Beun-dong Yuseong-gu, Daejeon 305-333, South Korea				, and E12.5 female mesonephros/gonad) and one newborn	
Tel: +82-42-860-4470				ovary cDNA library. Average insert size 1.5 kb. All	
Fax: +82-42-860-4409				source libraries are cloned unidirectionally with Oligo(dT	
Email: yongsung@email.kribb.re.kr				)-Not Primers. References include: (1) Genome-wide	
Plate: 12 row: H column: 12				expression profiling of mid-gestation placenta and embryo	
High quality sequence stcp: 538.				using a 15,000 mouse developmental cDNA microarray, 2000,	

FEATURES	source	BASE COUNT	150 a	/dev-stage="5 weeks"
location/Qualifiers				
1. .538				
/organism="Homo sapiens"				
/db_xref="taxon:9606"				
/clone="SSNU601-12-H12"				
/sex="M"				
/tissue_type="Ascites"				
/cell_type="Epithelial"				
/cell_line="SNL-601"				
/lab_host="Top10F"				
/note="Organ: Stomach; Vector: PME18-FL3; Site_1: XbaI;				
bacterial alkaline phosphatase (BAP) and then decapped				
with tobacco acid pyrophosphatase (TAP). The decapped				
intact mRNA was ligated with DNA-RNA linker including SfiI				
site by treatment of T4 RNA ligase and the first strand				
cDNA was synthesized with SuperScript II using SfiI				
Oligo-dT primer. After first strand synthesis, RNA was				
degraded by NaOH treatment and cDNA was amplified by PCR				
reaction. The PCR products were digested with SfiI and				
cloned into DRRII- digested pME18-FL3 vector. The				
obtained cDNA vectors were used for transformation of				
competent cells E. coli Top10F by electroporation method.				
The cDNA libraries constructed by this method are				
full-length enriched cDNA library."				
ORIGIN	196 a	104 c	102 g	136 t
BASE COUNT				
Alignment Scores:				
pred. No.:	1.26e+03	Length:	538	
Score:	41.00	Matches:	8	
Percent Similarity:	100.00%	Conservative:	1	
best local Similarity:	88.89%	Mismatches:	0	
Query Match:	93.18%	Indels:	0	
DB:	14	Gaps:	0	
US-09-698-781-17 (1-9) x BW751298 (1-538)				
Qy	1 ThrLeuPheProValLeuLeuPhLeu	9		
Db	48 AGGTGTTCCCTCTCTTCTG	22		
RESULT 8				
BE036163	BE036163	Mus musculus		
DEFINITION	575 bp mRNA	619 bp DNA	linear	GSS 09-MAY-2000
ACCESSION	BE036163	RPCI-23·69G20	TJB	RPCI-23 Mus musculus genomic clone
VERSION	BE036163.1	RPCI-23·469G20	TJB	RPCI-23·469G20, DNA sequence.
KEYWORDS		AZ108486.1	GI:7761463	
SOURCE		GSS.		
ORGANISM		Mus musculus		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 619)			
AUTHORS	Zhao,S., Nieman,W., Feldblum,T., Malek,J., Shatsman,S., Akinret, ,B., Devins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P., and Fraser,C.M.			
TITLE	Mouse BAC End Sequences from Library RPCI-23			
JOURNAL	Unpublished (1999)			
COMMENT	Other GSS: RPCI-23·469G20.TV Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0200 Email: szhao@tigr.org			
ORGANISM		Clonies are derived from the mouse BAC library RPCI-23. For BAC		
Mesembryanthemum crystallinum		library availability, Please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from		
Spermatophyta; Magnoliophyta; eudicots; core eudicots;		BACPAK Resources ( <a href="http://bacpac.med.buffalo.edu/orderframe.htm">http://bacpac.med.buffalo.edu/orderframe.htm</a> )		
Carophyllidae; Carophyllales; Aizoaceae; Mesembryanthemum.		or from Resea ch Genetics ( <a href="http://inforesgen.com">inforesgen.com</a> ). BAC end page: <a href="http://www.tigr.org/tigrdb/bac_ends/mouse/bac_end_intro.html">http://www.tigr.org/tigrdb/bac_ends/mouse/bac_end_intro.html</a>		
REFERENCE	1 (bases 1 to 575)	Plate: 469 row: G column: 20		
AUTHORS		Seq primer: SP6		
JOURNAL		Class: BAC ends		
COMMENT		Location/Qualifiers		
University of Arizona		1. .619		
Bio Sciences West room 513, Tucson, AZ 85721, USA		/organism="Mus musculus"		
Tel: 520-211-982		/strain="C57BL/6J"		
Fax: 520-621-1697		/db_xref="taxon:10090"		
Email: cbme.arizona.edu		/clone="RPCI-23·69G20"		
Location/Qualifiers		/clone.lib="RPCI-23"		
source		/sex="Female"		
FEATURES		/lab_host="B101B"		
ORGANISM		/note=Organ: Kidney/Brain; Vector: PBACE3; 6; Site_1: EcRI; Site_2: EcRI; Female C57BL/6J mouse kidney and/or		
clone.lib="MO"		brain genomic DNA was isolated and partially digested		
base_count	157 a	150 c	105 g	197 t
ORIGIN		selected DNA was cloned into the PBACE3 vector at the		
source		DH10B electrocompetent cells (BRL Life Technologies).		
FEATURES		EcRI sites. The ligation products were transformed into		
ORGANISM				
clone.lib="MO"				
tissue_type="apical meristem and leaf primordia"				



Email: cgabbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the T.M.A.G.E. Consortium/LINL at:

<http://image.llnl.gov/>

Plate: LLNL48463 row: m column: 04

High quality sequence stop: 689.

FEATURES  
Source

Location/Qualifiers

1. .724

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:3463851"

/clone\_1ib="NIH\_MGC\_12"

/tissue\_type="cervical carcinoma cell line"

/lab\_host="DH10B"

/note="Organ: cervix; Vector: pCMV-SPORT6; Site\_1: NotI;

Site\_2: SalI; Cloned unidirectionally; Primer: Oligo dT.

Average insert size 1.4 kb. Library prepared by Life

Technologies."

BASE COUNT  
ORIGIN

257 a 131 c 164 g 172 t

Alignment Scores:

Pred. No.: 1.81e+03

Length: 724

Score: 41.00

Matches: 8

Percent Similarity: 100.00%

Conservative: 1

Best Local Similarity: 88.89%

Mismatches: 0

Query Match: 93.18%

DB: 10

Gaps: 0

US-09-698-781-17 (1-9) x BE545083 (1-724)

QY 1 ThrieupheProValleuLeupheleu 9

Db 359 ACTCTCTTCCTCCTCTTTCT 36

RESULT 14

BM715733/c

LOCUS BM715733

DEFINITION UI-E-ED0-ahj-o-03-0-UI.r2 UI-E-ED0 Homo sapiens mRNA sequence.

ACCESSION BM715733

VERSION BM715733.1

KEYWORDS EST.

SOURCE

RESULT 13

BM013479

LOCUS BM013479

DEFINITION 603638933FL NIH\_MGC\_87 Homo sapiens cDNA clone IMAGE:5415056 5'

ACCESSION BM013479

VERSION BM013479.1

EST.

SOURCE

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 767)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 9704477

COMMENT Contact: Soares, MB

University of Iowa Program for Rat Gene Discovery and Mapping

451 Echstein Medical Research Building Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: msoares@blue.weeg.uiowa.edu

/lab\_host="DH10B (phage-resistant)"

/note="Organ: breast; Vector: pCMV-SPORT6; Site\_1: NotI;

Site\_2: SalI; Cloned unidirectionally; Oligo-dT primed.

Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies.

Note: this is a NIH\_MGC library."

BASE COUNT  
ORIGIN

237 a 174 c 207 g 149 t

Alignment Scores:

Pred. No.: 1.95e+03

Length: 767

Score: 41.00

Matches: 8

Percent Similarity: 100.00%

Conservative: 1

Best Local Similarity: 88.89%

Mismatches: 0

Query Match: 93.18%

DB: 13

Gaps: 0

US-09-698-781-17 (1-9) x BM013479 (1-767)

QY 1 ThrieupheProValleuLeupheleu 9

Db 62 ACTCTCTTCCTCCTCTTTCT 36

RESULT 14

BM715733/c

LOCUS BM715733

DEFINITION UI-E-ED0-ahj-o-03-0-UI.r2 UI-E-ED0 Homo sapiens mRNA sequence.

ACCESSION BM715733

VERSION BM715733.1

KEYWORDS EST.

SOURCE

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 767)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 9704477

COMMENT Contact: Soares, MB

University of Iowa Program for Rat Gene Discovery and Mapping

451 Echstein Medical Research Building Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: msoares@blue.weeg.uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

CDNA Library preparation: Dr. M. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics ([www.resgen.com](http://www.resgen.com)).

The following repetitive elements were found in this cDNA

sequence: 254-301 >(GAA)nSimple\_repeat

Seq primer: M13 Reverse.

FEATURES  
Source

Location/Qualifiers

1. .785

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="DH10B-ahj-o-03-0-UI"

/clone\_1ib="UI-E-ED0"

/tissue\_type="retina, lens, eye anterior segment, optic nerve, retina and macula, RPE and choroid"

/dev\_stage="fetal and adult"

/lab\_host="DH10B (Life Technologies) T1 phage resistant"

/note="Organ: eye; Vector: pT7T3Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I;"

modified polylinker; Site\_1: EcoR I; Site\_2: Not I;

according to Bonaldo, Lennon and Soares, Genome Research,

6:791-806, 1996. First strand cDNA synthesis was primed

with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7Tn-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGATCAAGA ; lens, CGATAGCGA; optic nerve, CCATTAACG; retina, CCGGG; Retina Pveal and Macular, GTC; and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

BASE COUNT  
ORIGIN  
254 a  
185 c  
227 g  
116 t  
3 others

Alignment Scores:  
Pred. No.: 2.01e+03  
Score: 41.00  
Percent Similarity: 100.00%  
Best Local Similarity: 88.89%  
Query Match: 93.18%  
DB: 14  
Db 287 ACTCTCTTCTCTCTTCTTCTT 261

U.S.-09-698-781-17 (1-9) x BM715733 (1-785)

QY 1 ThreupheProvalLeuleupheleu 9  
||||||||:::|||||:|||||:|||||

Gaps: 0

Pred. No.: 2.09e+03  
Score: 41.00  
Percent Similarity: 100.00%  
Best Local Similarity: 88.89%  
Query Match: 93.18%  
DB: 31 ACTCTCTTCTCTCTCTCTTCTT 5

Search completed: March 14, 2003, 05:26:20  
Job time : 97.291 secs

RESULT 15  
LOCUS BG574770/c  
DEFINITION BG2596022F1 NIH\_MGC\_87 Homo sapiens mRNA clone IMAGE:4705685 5', mRNA sequence.  
ACCESSION BG574770  
VERSION BG574770.1  
KEYWORDS EST  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE I (bases 1 to 813)  
AUTHORS NIH-MGC  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgsbs@mail.nih.gov  
Tissue Procurement: BCTD/btp  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://Image.llnl.gov>  
Plate: LIAM0572 row: 1 column: 06  
High quality sequence stop: 801.

#### FEATURES

SOURCE  
1. .813  
/organism="Homo sapiens"  
/db\_xref=taxon:9606  
/clone="IMAGE:4705685"  
/clone.lib="NIH\_MGC\_87"  
/tissue\_type="mammary adenocarcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/note="organ: breast; Vector: pCMV-Sport6; Site\_1: NotI;  
Site\_2: SacI; Cloned unidirectionally; oligo-dT primed."  
Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies.  
Note: this is a NIH\_MGC Library.

BASE COUNT  
ORIGIN  
247 a  
180 c  
223 g  
163 t

Alignment Scores: